A SIMPLE PROCEDURE FOR CONSTRUCTING RESOLVABLE ROW-COLUMN EXPERIMENT DESIGNS

by

Walter T. Federer

Abstract

A method is described for constructing connected resolvable row-column experiment designs for v = ks treatments in s rows and k columns in each complete block. The optimality of the constructed designs is compared with those obtained using the software package GENDEX. Since the design optimality does not reach those obtained from the package, suggestions are made for improving the method. The method is illustrated using two examples, i.e., for v = 30, k = 5, and s = 6 and for v = 228, k = 12, and s = 19. Some comments on designing experiments are given in the last section.

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1. Introduction

A simple and straightforward method for constructing optimal resolvable incomplete block designs, RIBDs, has been described by Federer (1995). This method is an innovation of the one described by Khare and Federer (1981). A similar procedure is needed for resolvable row-column (lattice rectangle) designs, RRCDs. A simple and easy method for constructing RRCDs is illustrated via two examples, one for $v = 30$ treatments in $s = 6$ rows and $k = 5$ columns and the other for $v = 228$ treatments in $s = 19$ rows and $k = 12$ columns. There is software, e.g., GENDEX, available for constructing many resolvable row-column designs but situations arise in practice where the required plan is unavailable and needs to be constructed. In due time, software may become available to handle all situations arising in practice but until then a method for constructing RRCDs is needed. Such a method follows.

2. Construction of Incomplete Block Designs

The method used to construct resolvable incomplete block designs, RIBDs, is a modification of the "diagonalization" procedure of Khare and Federer (1981). To illustrate, we shall use $v = 30$ treatments in $s = 6$ incomplete blocks of size $k = 5$ in $r = 6$ complete blocks (replicates). The plan for the first replicate is obtained by writing the 30 numbers in a 6-row by 5-column array as follows:

Replicate 1

1	7	13	19	25
2	8	14	20	26
3	9	15	21	27
4	10	16	22	28
5	11	17	23	29
6	12	18	24	30

The rows of the above array form the $s = 6$ incomplete blocks of replicate 1.

To form a second replicate, use the main right diagonal, 1, 8, 15, 22, and 29, to form the first incomplete block of replicate 2. The remaining numbers in each column of replicate 1 are treated as an endless chain and entered cyclically in the columns of replicate 2 as follows:

Replicate 2

1	8	15	22	29
2	9	16	23	30
3	10	17	24	25
4	11	18	19	26
5	12	13	20	27
6	7	14	21	28

The main right diagonal of replicate 2 array is 1, 9, 17, 19, and 27. Since it is desired, if possible, to have an incomplete block design, IBD, with only two association classes, 0 or 1, in order to do this and since the number 19 has already occurred with number 1 in replicate 1, we adjust or modify the diagonal to be 1, 9, 17, 20, and 28, i.e., the diagonal dropped to number 20. These numbers form the first incomplete block of replicate 3 and proceeding as above replicate 3 is:

Replicate 3

1	9	17	20	28
2	10	18	21	29
3	11	13	22	30
4	12	14	23	25
5	7	15	24	26
6	8	16	19	27

Using the stepped-down right "diagonal" of 1, 10, 14, 24, and 27 and the above procedure, replicate 4 is formed as:

Replicate 4

1	10	14	24	27
2	11	15	19	28
3	12	16	20	29
4	7	17	21	30
5	8	18	22	25
6	9	13	23	26

Now use the stepped-down right "diagonal" of 1, 11, 16, 21, and 26 to form replicate 5 as follows:

Replicate 5

1	11	16	21	26
2	12	17	22	27
3	7	18	23	28
4	8	13	24	29
5	9	14	19	30
6	10	15	20	25

The modified right diagonal of 1, 12, 18, 23, and 30 forms the first incomplete block of replicate 6 which is:

Replicate 6				
1	12	18	23	30
2	7	13	24	25
3	8	14	19	26
4	9	15	20	27
5	10	16	21	28
6	11	17	22	29

Treatments 1 to 6 have only two association classes $\lambda_1 = 0$ and $\lambda_2 = 1$ for $v = 30$ treatments in incomplete blocks of size $k = 5$ and with $r = 6$ complete blocks. There are $n_1 = 24$ treatments that occur in an incomplete block with a given treatment and $n_0 = 5$ treatments which do not appear in an incomplete block with the given treatment for treatments 1 to 6. This association scheme does not hold for the other treatments. For example, treatment number 1 occurs once in an incomplete block with treatments 7 to 30 and does not occur with treatments 2 to 6. This is as near-balanced design as can be obtained for treatment 1.

3. Construction of Resolvable Row-Column Designs

To construct a RRCD, a RIBD is obtained first as described above. The first replicate of the RRCD is the above replicate 1. To obtain replicate 2, the numbers within a row are cyclically moved to obtain the RRCD. For the above RIBD and replicate 1, replicate 1 of the RRCD is the same column arrangement as in section 2. For replicate 2, the numbers in column 1 of replicate 1 are 1, 2, 3, 4, 5 and 6. Ignoring the number 1 consider the remaining numbers to be on an endless chain which will be rotated one position for each additional replicate on the main right diagonal. The numbers within a row, incomplete block are also considered to be on an endless chain. The numbers 2, 3, 4, 5, and 6 are moved one position to obtain the number 6 in row 2 and column 1; the number 2 appears in row 3 and column 2; the number 3 appears in row 4 and column 3; etc. The second replicate is formed with rows 1 and 6 the same as replicate 2 of section 2. The cyclic rotation of numbers on an endless chain in the rows is followed to obtain replicate 2:

Replicate 2				
1	8	15	22	29
6	7	14	21	28
30	2	9	16	23
24	25	3	10	17
18	19	26	4	11
12	13	20	27	5

Replicate 3 of the RRCD is formed from replicate 3 of section 2 as follows where rows 1 and 5 are the same as replicate 3 of section 2. The numbers 6, 2, 3, 4, and 5 are rotated one position on the main right diagonal to have 5 in row 2:

Replicate 3

1	9	17	20	28
5	7	15	24	26
27	6	8	16	19
21	29	2	10	18
13	22	30	3	11
12	14	23	25	4

Replicate 4 of the RRCD is formed by rotation of the numbers 5, 6, 2, 3, and 4 one position in the main right diagonal resulting in rows 1 and 4 being the same as replicate 4 of section 2 and is:

Replicate 4

1	10	14	24	27
4	7	17	21	30
25	5	8	18	22
23	26	6	9	13
15	19	28	2	11
12	16	20	29	3

Replicate 5 of the RRCD is formed from replicate 5 of the previous section by rotating the numbers 4, 5, 6, 2, and 3 one position resulting in rows 1 and 3 being the same as replicate 5 of section 2 and is:

Replicate 5

1	11	16	21	26
3	7	18	23	28
29	4	8	13	24
19	30	5	9	14
15	20	25	6	10
12	17	22	27	2

Replicate 6 of the RRCD is formed from replicate 6 of the previous section by rotating the numbers 3, 4, 5, 6, and 2 one position in the main right diagonal resulting in rows 1 and 2 being the same as in replicate 6 of section 2 and is:

Replicate 6

1	12	18	23	30
2	7	13	24	25
26	3	8	14	19
20	27	4	9	15

16	21	28	5	10
11	17	22	29	6

For the above six replicates of an RRCD, the association scheme in rows is the same as in section 2. The association scheme in columns has treatments occurring together $\lambda_1 = 0$ times, $\lambda_2 = 1$ times, $\lambda_3 = 2$ times, $\lambda_4 = 3$ times, and $\lambda_5 = 4$ times to produce a five association scheme design for columns. The treatment-column incidence matrix is:

10000	10000	10000	10000	10000	10000
10000	01000	00100	00010	00001	10000
10000	00100	00010	00001	10000	01000
10000	00010	00001	10000	01000	00100
10000	00001	10000	01000	00100	00010
10000	10000	01000	00100	00010	00001
01000	01000	01000	01000	01000	01000
01000	01000	00100	00100	00100	00100
01000	00100	01000	00010	00010	00010
01000	00010	00010	01000	00001	00001
01000	00001	00001	00001	01000	10000
01000	10000	10000	10000	10000	01000
00100	01000	10000	00001	00010	00100
00100	00100	01000	00100	00001	00010
00100	00100	00100	10000	10000	00001
00100	00010	00010	01000	00100	10000
00100	00001	00100	00100	01000	01000
00100	10000	00001	00010	00100	00100
00010	01000	00001	01000	10000	00001
00010	00100	00010	00100	01000	10000
00010	00010	10000	00010	00010	01000
00010	00010	01000	00001	00100	00100
00010	00001	00100	10000	00010	00010
00010	10000	00010	00010	00001	00010
00001	01000	00010	10000	00100	00001
00001	00100	00001	01000	00001	10000
00001	00010	10000	00001	00010	01000
00001	00001	00001	00100	00001	00100
00001	00001	01000	00010	10000	00010
00001	10000	00100	00001	01000	00001

The above matrix times its transpose, the association matrix, is a 30 by 30 matrix with r = 6 on the diagonal and 0, 1, 2, 3, or 4 elsewhere. As stated above, this is a five associate class design with regard to the treatment-column association. It is a three associate class design for treatment-row association.

Either the design in this section or the one in section 2 could have been obtained using a software package such as GENDEX. The number of zeroth associates, first associates, and second associates obtained by GENDEX and for the above RRCD design are discussed in section 5.

4. An RRCD for v = 228

A member of the Department of Plant Breeding wished to have an experiment design for v = 228 varieties and r = 5 replicates. One could have used any of the following:
Incomplete block size k= 2
Incomplete block size k = 4
Incomplete block size k = 6
Incomplete block size k = 12
Incomplete block size k = 19
Incomplete block size k = 38
Incomplete block size k = 57
Incomplete block size k = 76
Complete block size k = 228
The experimenter opted to use k = 4 and the design was obtained using the method of section 2. These designs could have been obtained using the ALPHA module of GENDEX.

A possibly better alternative to any of the above would be to use a RRCD of 19 rows by 12 columns. Such a design does not exist but may be constructed using the procedure of section 3. Replicate 1 of a RRCD for v = 228, k = 12 columns, and s = 19 rows is:

Replicate 1

1	20	39	58	77	96	115	134	153	172	191	210
2	21	40	59	78	97	116	135	154	173	192	211
3	22	41	60	79	98	117	136	155	174	193	212
4	23	42	61	80	99	118	137	156	175	194	213
5	24	43	62	81	100	119	138	157	176	195	214
6	25	44	63	82	101	120	139	158	177	196	215
7	26	45	64	83	102	121	140	159	178	197	216
8	27	46	65	84	103	122	141	160	179	198	217
9	28	47	66	85	104	123	142	161	180	199	218
10	29	48	67	86	105	124	143	162	181	200	219
11	30	49	68	87	106	125	144	163	182	201	220
12	31	50	69	88	107	126	145	164	183	202	221
13	32	51	70	89	108	127	146	165	184	203	222
14	33	52	71	90	109	128	147	166	185	204	223
15	35	53	72	91	110	129	148	167	186	205	224
16	36	54	73	92	111	130	149	168	187	206	225
17	37	55	74	93	112	131	150	169	188	207	226
18	38	56	75	94	113	132	151	170	189	208	227

19	39	57	76	95	114	133	152	171	190	209	228

Replicate 2 of the RRCD is formed by first constructing a second replicate for a RIBD using the diagonal 1, 21, 41, 61, 81, 101, 121, 141, 161, 181, 201, and 221. Then since there are only 12 columns, eight of the 19 numbers in each column of the RIBD will need to remain the same for the RRCD. Leaving row 1 unchanged in all replicates, the numbers 2 to 19 will be considered as an endless chain to be rotated through 18 - 11 = 7 rows of column 1 and in the main right diagonal below row 8. Performing this operation leaves the numbers 13-19 in column 1, number 1 in row 9 and column 2, number 2 in row 10 and column 3, etc. so that the numbers 2-12 appear on the diagonal. The treatments within a row remain the same as in the RIBD but are rotated in the row according to where the lowest number in a row falls on the diagonal. Performing these operations, the second replicate of the RRCD is:

Replicate 2

1	21	41	61	81	101	121	141	161	181	201	221
13	33	53	73	93	113	133	134	154	174	194	214
14	34	54	74	94	114	115	135	155	175	195	215
15	35	55	75	95	76	116	136	156	176	196	216
16	36	56	76	77	97	117	137	157	177	197	217
17	37	57	58	78	98	118	138	158	178	198	218
18	38	39	59	79	99	119	139	159	179	199	219
19	20	40	60	80	100	120	140	160	180	200	220
222	2	22	42	62	82	102	122	142	162	182	202
203	223	3	23	43	63	83	103	123	143	163	183
184	202	224	4	24	44	64	84	104	124	144	164
165	185	205	225	5	25	45	65	85	105	125	145
146	166	186	206	226	6	26	46	66	86	106	126
127	147	167	187	207	227	7	27	47	67	87	107
108	128	148	168	188	208	228	8	28	48	68	88
89	109	129	149	169	189	209	210	9	29	49	69
70	90	110	130	150	170	190	191	211	10	30	50
51	71	91	111	131	151	171	172	192	212	11	31
32	52	72	92	112	132	152	153	173	193	213	12

To form replicate 3, obtain replicate 3 of an IBD as explained in section 2. The diagonal used is the first row of the following square. Then keep rows 6 to 12 the same as in the IBD (i.e., numbers 6 to 12 appear in column 1) and move the numbers in the remaining rows one position to the right of the previous row. Performing these operations, replicate 3 is formed as:

Replicate 3

1	22	43	64	85	106	127	148	169	190	192	213
6	27	48	69	90	111	132	134	155	176	197	218
7	28	49	70	91	112	133	135	156	177	198	219
8	29	50	71	92	113	115	136	157	178	199	220

9	30	51	72	93	114	116	137	158	179	200	221
10	31	52	73	94	96	117	138	159	180	201	222
11	32	53	74	95	97	118	139	160	181	202	223
12	33	54	75	77	98	119	140	161	182	203	224
225	13	34	55	76	78	99	120	141	162	183	204
205	226	14	35	56	58	79	100	121	142	163	184
185	206	227	15	36	57	59	80	101	122	143	164
165	186	207	228	16	37	39	60	81	102	123	144
145	166	187	208	210	17	38	40	61	82	103	124
125	146	167	188	209	211	18	20	41	62	83	104
105	126	147	168	189	191	212	19	21	42	63	84
86	107	128	149	170	172	193	214	2	23	44	65
66	87	108	129	150	171	173	194	215	3	24	45
46	67	88	109	130	151	134	174	195	216	4	25
26	47	68	89	110	131	152	154	175	196	217	5

The IBD plan for replicate 4 is obtained as described in section 2. To maximize pairwise balance of association, rows 17 to 19 and 2 to 5 will not have the numbers moved one position to the right and will appear in column 1. Rows 6 to 16 will appear on the diagonal of rows 9 to 19. These operations result in the following row and column arrangements:

Replicate 4

1	23	45	67	89	111	133	136	158	180	202	224
17	20	42	64	86	108	130	152	155	177	199	221
18	21	43	65	87	109	131	134	156	178	200	222
19	22	44	66	88	110	132	135	157	179	201	223
2	24	46	68	90	112	115	137	159	181	203	225
3	25	47	69	91	113	116	138	160	182	204	226
4	26	48	70	92	114	117	139	161	183	205	227
5	27	49	71	93	96	118	140	162	184	206	228
210	6	28	50	72	94	97	119	141	163	185	207
208	211	7	29	51	73	95	98	120	142	164	186
187	209	212	8	30	52	74	77	99	121	143	165
166	188	191	213	9	31	53	75	78	100	122	144
145	167	189	192	214	10	32	54	76	79	101	123
124	146	168	190	193	215	11	33	55	58	80	102
103	125	147	169	172	194	216	12	34	56	59	81
82	104	126	148	170	173	195	217	13	35	57	60
61	83	105	127	149	171	174	196	218	14	36	39
40	62	84	106	128	150	153	175	197	219	15	37
38	41	63	85	107	129	151	154	176	198	220	16

Replicate 5 is formed similar to replicate 5 in section 2 with a stepped-down diagonal. Rows 10 to 16 are not permuted but left the same. Rows 17 to 19 and rows 2

to 9 are moved one position on the diagonal to the right from the previous one as above. These operations result in the following:

Replicate 5

1	24	47	70	93	98	122	145	168	173	196	219
10	33	56	60	83	107	131	135	158	182	205	228
11	34	57	61	84	108	132	136	159	183	206	210
12	35	39	62	85	109	133	137	160	184	207	211
13	36	40	63	86	110	115	138	161	185	208	212
14	37	41	64	87	111	116	139	162	186	209	213
15	38	42	65	88	112	117	140	163	187	191	214
16	20	43	66	89	113	118	141	164	188	192	215
216	17	21	44	67	90	114	119	142	165	189	193
194	217	18	22	45	68	91	96	120	143	166	190
172	195	218	19	23	46	69	92	97	121	144	167
169	174	197	220	2	25	48	71	94	99	123	146
147	170	175	198	221	3	26	49	72	95	100	124
125	148	171	176	199	222	4	27	50	73	77	101
102	126	149	153	177	200	223	5	28	51	74	78
79	103	127	150	154	178	201	224	6	29	52	75
76	80	104	128	151	155	179	202	225	7	30	53
54	58	81	105	129	152	156	180	203	226	8	31
32	55	59	82	106	130	134	157	181	204	227	9

5. Comparison of Design with Those Obtained From GENDEX

Using the BIB module in GENDEX, a RIBD for $v = 30$ and $k = 5$ in $r = 6$ replicates was obtained. There were 92 zeroth (i.e., numbers did not occur together in any incomplete block (row)), 350 first associates (a pair of treatment numbers occurred together in one of the incomplete blocks), and 16 second associates (a pair of treatment numbers occurred together in two incomplete blocks). This design reached 99.53% of the upper bound possible, i.e., the design was nearly optimal. Using the ALPHA module, a RIBD for $v = 30$ and $k = 5$ with $r = 6$ replicates, there were 99 zeroth associates, 312 first associates, and 24 second associates. The relative efficiency of this design was 99.36%, slightly lower than for the BIB module design. For the RIBD as constructed in this paper, there were 123 zeroth associates, 264 first associates, and 48 second associates. The design with the highest efficiency will be the one with the fewest associate classes and with most of the pairings falling one class. Here the design from the BIB module has 350 first associates out of the 435 possible pairs. If there is only one associate class, the RIBD is a balanced incomplete block design.

The method used to construct the RIBD of this paper was attempting to have only two associate classes. This was achieved for numbers 1 to 6 each of which have 5 zeroth associates and 24 first associates. Numbers 7 to 12 each had 10 zeroth associates, 14 first associates, and 5 second associates. Numbers 13 to 18 each had 8 zeroth associates, 18 first associates, and 3 second associates. Numbers 19 to 30 each had 9 zeroth associates, 16 first associates, and 4 second associates. A design with this imbalance in associate

numbers in the classes would be less efficient relative to intrablock efficiency but when interblock information is recovered much of the loss in efficiency is negated (Federer and Speed, 1987).

For the RIBD with $v = 30$, $k = 6$, and $r = 6$, the BIB module of GENDEX produced a design with 64 zeroth associates, 293 first associates, 77 second associates, and 1 third associates (one pair of treatment numbers occurred together in three of the 30 incomplete blocks). The efficiency of the design relative to the upper bound was 99.90%. The ALPHA module of GENDEX produced a design with 75 zeroth associates, 270 first associates, and 90 second associates with an efficiency of 99.77%. The RIBD constructed by the method of section 2 had 93 zeroth associates, 243 first associates, 92, second associates, 5 third associates, and 2 fourth associates. The pairwise association of treatments was not as good as for those designs obtained from GENDEX. There was considerable imbalance of pairing associations of treatment numbers ranging from three classes of associates to five classes. Treatment numbers 5 and 6 exhibited the best balance with all the other treatment numbers. Comparison of the RRCD for $v = 30$ treatments as obtained above may be made with the ones obtained via GENDEX using the BIB, ALPHA, and RRCD modules.

6. Some Comments

It may be possible to refine the procedure described herein. One possibility is to use a main right diagonal rather than a modified one. This may correct the most of the imbalance in pairings and could improve the efficiency of the design. Another possibility for improving the efficiency and balance is to use more than one diagonal and perhaps switch between right and left diagonals when constructing plans for successive replicates.

Fisher (1949) stated, "If experimentation were only concerned with the comparison of four to eight treatments or varieties, it (the Latin square) would therefore be not merely the principal but almost the universal design employed". This statement implies that row-column designs should be used whenever possible. Yates (1940) with the development of lattice square designs solved the problem for $v = k^2$ treatments still using the Latin principle. Since that time row-column designs (lattice rectangle designs) for $v = ks$ treatments have become available and even incorporated into software packages (e. g., GENDEX). Hence there is little excuse for not using lattice rectangle designs unless the experimenter is certain that an IBD will control the variation present in an experiment. When analyzing the results from designed experiments, the analyst should be careful to select an appropriate model. Standard textbook analyses may be inappropriate for many designed experiments as shown by Federer (1998).

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